

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/567,486
Source: IFP
Date Processed by STIC: 2/13/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/567,486

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 02/13/2006

PATENT APPLICATION: US/10/567,486

TIME: 12:41:39

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02132006\J567486.raw

*see item 2 on Even
Summary Sheet*

3 <110> APPLICANT: CIPOLLONE, Francesco et al
5 <120> TITLE OF INVENTION: Method and kit for assessing the risk of cardiovascular pathologies with

6 atheromatous etiology

8 <130> FILE REFERENCE: NOTAR9.001APC

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/567,486

C--> 10 <141> CURRENT FILING DATE: 2006-02-06

10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/051711

11 <151> PRIOR FILING DATE: 2004-08-04

12 <150> PRIOR APPLICATION NUMBER: IT MI2003A001607

14 <151> PRIOR FILING DATE: 2003-08-05

16 <160> NUMBER OF SEQ ID NOS: 4

18 <170> SOFTWARE: PatentIn version 3.3

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 1400

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

26 <220> FEATURE:

27 <221> NAME/KEY: CDS

28 <222> LOCATION: (1335)..(1400)

29 <223> OTHER INFORMATION: Homo sapiens cyclooxygenase-2 (PTGS2) gene corresponding to
30 Genbank accession number AF276953. Nucleotide in position 1371

31 can also be "t" or "g" or "c" Nucleotide polymorphism detected

32 on position 436, according to what?

35 <400> SEQUENCE: 1

36	ttccagctgt	caaaatctcc	cttccatcta	attaattcct	catccaacta	tgttccaaaa	60
38	cgagaataga	aaattagccc	caataagccc	aggcaactga	aaagtaaagt	ctatgttgta	120
40	ctttgatcca	tggtcacaac	tcataatctt	ggaaaagtgg	acagaaaaga	caaaagagtg	180
42	aactttaaaa	ctcgaattta	ttttaccagt	atctcctatg	aagggctagt	aaccaaata	240
44	atccacgcat	cagggagaga	aatgccttaa	ggcatacggt	ttggacattt	agcgtccctg	300
46	caaattctgg	ccatcgccgc	ttcctttgtc	catcagaagg	caggaaactt	tatattggtg	360
48	acccgtggag	ctcacattaa	ctattttacag	ggtaactgct	taggaccagt	attatgagga	420
50	gaattttacct	ttcccgccctc	tcttttccaag	aaacaaggag	ggggtgaagg	tacggagaac	480
52	agtattttctt	ctgttgaaag	caacttagct	acaaagataa	attacagcta	tgtacactga	540
54	aggtagctat	ttcattccac	aaaataagag	ttttttaaaa	agctatgtat	gtatgtgctg	600
56	catatagagc	agatatacag	cctattaagc	gtcgtcacta	aaacataaaa	catgtcagcc	660
58	tttcttaacc	ttactcgccc	cagtctgtcc	cgacgtgact	tcctcgaccc	tctaaagacg	720
60	tacagaccag	acacggcggc	ggcggcgggg	gaggggattc	cctgcgcccc	cggacctcag	780
62	ggccgctcag	attcctggag	aggaagccaa	gtgtcctttc	gccctcccc	ggtatcccat	840
64	ccaaggcgat	cagtcacaga	ctggctctcg	gaagcgctcg	ggcaaagact	gcgaagaaga	900
66	aaagacactct	ggcgggaaacc	tgtgcgcctg	gggcggtgga	actcggggag	gagagggagg	960
68	gatcagacag	gagagtgggg	actacccctc	ctgctcccaa	attggggcag	cttctctgggt	1020
70	ttccgatttt	ctcattttccg	tgggtaaaaa	accctgcccc	caccgggctt	acgcaatttt	1080
72	tttaagggga	gaggagggga	aaatttgtgg	ggggtacgaa	aaggcggaaa	gaaacagtca	1140

*Does Not Comply
Corrected Diskette Needed*

pp 1-2

*"a" (at
location
1371)*

*Can only
represent
itself. Use
"n" instead,
and
explain in
<2207-2223>
section*

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Input Set : A:\pto.da.txt

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```

74 tttcgtcaca tgggcttggt tttcagtcctt ataaaaagga aggttctctc ggtagcgac 1200
76 caattgtcat acgacttgca gtgagcgtca ggagcacgtc caggaactcc tcagcagcgc 1260
78 ctcccttcagc tccacagcca gacgccttca gacagcaaag cctacccccg cgccgcgccc 1320
80 tgccccgcgc tgcg atg ctc gcc cgc gcc ctg ctg ctg tgc gcg gtc ctg 1370
81 Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu
82 1 5 10
84 acg ctc agc cat aca ggt gag tac ctg gcg 1400
85 Thr Leu Ser His Thr Gly Glu Tyr Leu Ala
86 15 20
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 22
91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
94 <400> SEQUENCE: 2
96 Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Thr Leu Ser His
97 1 5 10 15
100 Thr Gly Glu Tyr Leu Ala
101 20
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 20
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapiens
110 <220> FEATURE:
111 <221> NAME/KEY: primer_bind
112 <222> LOCATION: (1)..(20)
114 <400> SEQUENCE: 3
115 ccgcttcctt tgtccatcag 20
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 21
120 <212> TYPE: DNA
121 <213> ORGANISM: Homo sapiens
124 <220> FEATURE:
125 <221> NAME/KEY: primer_bind
126 <222> LOCATION: (1)..(21)
128 <400> SEQUENCE: 4
129 gctatgtaca ctgaaggtag c 21

```

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 02/13/2006

PATENT APPLICATION: US/10/567,486

TIME: 12:41:40

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02132006\J567486.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/567,486

DATE: 02/13/2006

TIME: 12:41:40

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02132006\J567486.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date